RAW SEQUENCE LISTING
ERROR REPORT

BIO●HNOLOGY
SYSTEMS
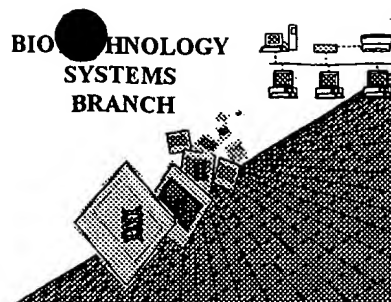BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/701,395_

Source: _PCT 09_

Date Processed by STIC: _1/23/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

PCT09

```
                RAW SEQUENCE LISTING           DATE: 01/23/2001
                PATENT APPLICATION:  US/09/701,395    TIME: 11:13:18

                   Input Set : A:\108172-00022.txt
                   Output Set: N:\CRF3\01232001\I701395.raw
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     4 <110> APPLICANT: CUNNINGHAM JR., FRANCIS X.
     5        SUN, ZAIREN
     7 <120> TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
     8        METHODS OF USE THEREOF
    10 <130> FILE REFERENCE: 8172-9023
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/701,395
C--> 13 <141> CURRENT FILING DATE: 2000-12-04
    15 <150> PRIOR APPLICATION NUMBER: 09/088,724
    16 <151> PRIOR FILING DATE: 1998-06-02
    18 <150> PRIOR APPLICATION NUMBER: 09/088,725
    19 <151> PRIOR FILING DATE: 1998-06-02
    21 <160> NUMBER OF SEQ ID NOS: 61
    23 <170> SOFTWARE: PatentIn Ver. 2.0
    25 <210> SEQ ID NO: 1
    26 <211> LENGTH: 1860
    27 <212> TYPE: DNA
    28 <213> ORGANISM: Arabidopsis thaliana
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    38                                                       Met Glu Cys
    39                                                        1
    41 gtt ggg gct agg aat ttc gca gca atg gcg gtt tca aca ttt ccg tca   165
    42 Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr Phe Pro Ser
    43  5                  10                  15
    45 tgg agt tgt cga agg aaa ttt cca gtg gtt aag aga tac agc tat agg   213
    46 Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr Ser Tyr Arg
    47  20                  25                  30                  35
    49 aat att cgt ttc ggt ttg tgt agt gtc aga gct agc ggc ggc gga agt   261
    50 Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly Gly Gly Ser
    51                  40                  45                  50
    53 tcc ggt agt gag agt tgt gta gcg gtg aga gaa gat ttc gct gac gaa   309
    54 Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe Ala Asp Glu
    55                  55                  60                  65
    57 gaa gat ttt gtg aaa gct ggt ggt tct gag att cta ttt gtt caa atg   357
    58 Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe Val Gln Met
    59                  70                  75                  80
    61 cag cag aac aaa gat atg gat gaa cag tct aag ctt gtt gat aag ttg   405
    63 Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val Asp Lys Leu
    64  85                  90                  95
    66 cct cct ata tca att ggt gat ggt gct ttg gat cat gtg gtt att ggt   453
    67 Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val Val Ile Gly
    68 100                 105                 110                 115
    70 tgt ggt cct gct ggt tta gcc ttg gct gca gaa tca gct aag ctt gga   501
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71 Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala Lys Leu Gly
72            120                 125                 130
74 tta aaa gtt gga ctc att ggt cca gat ctt cct ttt act aac aat tac     549
75 Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr
76            135                 140                 145
78 ggt gtt tgg gaa gat gaa ttc aat gat ctt ggg ctg caa aaa tgt att     597
79 Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln Lys Cys Ile
80            150                 155                 160
82 gag cat gtt tgg aga gag act att gtg tat ctg gat gat gac aag cct     645
83 Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp Asp Lys Pro
84     165                 170                 175
86 att acc att ggc cgt gct tat gga aga gtt agt cga cgt ttg ctc cat     693
87 Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg Leu Leu His
88 180                 185                 190                 195
90 gag gag ctt ttg agg agg tgt gtc gag tca ggt gtc tcg tac ctt agc     741
91 Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser Tyr Leu Ser
92            200                 205                 210
94 tcg aaa gtt gac agc ata aca gaa gct tct gat ggc ctt aga ctt gtt     789
95 Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu Arg Leu Val
96            215                 220                 225
98 gct tgt gac gac aat aac gtc att ccc tgc agg ctt gcc act gtt gct     837
99 Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala Thr Val Ala
100            230                 235                 240
102 tct gga gca gct tcg gga aag ctc ttg caa tac gaa gtt ggt gga cct    885
103 Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val Gly Gly Pro
104            245                 250                 255
106 aga gtc tgt gtg caa act gca tac ggc gtg gag gtt gag gtg gaa aat    933
107 Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu Val Glu Asn
108 260                 265                 270                 275
110 agt cca tat gat cca gat caa atg gtt ttc atg gat tac aga gat tat    981
111 Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr Arg Asp Tyr
112            280                 285                 290
114 act aac gag aaa gtt cgg agc tta gaa gct gag tat cca acg ttt ctg    1029
115 Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro Thr Phe Leu
116            295                 300                 305
118 tac gcc atg cct atg aca aag tca aga ctc ttc ttc gag gag aca tgt    1077
119 Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu Glu Thr Cys
120            310                 315                 320
122 ttg gcc tca aaa gat gtc atg ccc ttt gat ttg cta aaa acg aag ctc    1125
123 Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys Thr Lys Leu
125            325                 330                 335
127 atg tta aga tta gat aca ctc gga att cga att cta aag act tac gaa    1173
128 Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys Thr Tyr Glu
129 340                 345                 350                 355
131 gag gag tgg tcc tat atc cca gtt ggt ggt tcc ttg cca aac acc gaa    1221
132 Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro Asn Thr Glu
133            360                 365                 370
135 caa aag aat ctc gcc ttt ggt gct gcc gct agc atg gta cat ccc gca    1269
136 Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val His Pro Ala
```

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137               375                   380                   385
139 aca ggc tat tca gtt gtg aga tct ttg tct gaa gct cca aaa tat gca        1317
140 Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro Lys Tyr Ala
141           390                   395                   400
143 tca gtc atc gca gag ata cta aga gaa gag act acc aaa cag atc aac        1365
144 Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys Gln Ile Asn
145       405                   410                   415
147 agt aat att tca aga caa gct tgg gat act tta tgg cca cca gaa agg        1413
148 Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro Pro Glu Arg
149 420                   425                   430                   435
151 aaa aga cag aga gca ttc ttt ctc ttt ggt ctt gca ctc ata gtt caa        1461
152 Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln
153                   440                   445                   450
155 ttc gat acc gaa ggc att aga agc ttc ttc cgt act ttc ttc cgc ctt        1509
156 Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe Phe Arg Leu
157               455                   460                   465
159 cca aaa tgg atg tgg caa ggg ttt cta gga tca aca tta aca tca gga        1557
160 Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu Thr Ser Gly
161           470                   475                   480
163 gat ctc gtt ctc ttt gct tta tac atg ttc gtc att tca cca aac aat        1605
164 Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser Pro Asn Asn
165       485                   490                   495
167 ttg aga aaa ggt ctc atc aat cat ctc atc tct gat cca acc gga gca        1653
168 Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro Thr Gly Ala
169 500                   505                   510                   515
171 acc atg ata aaa acc tat ctc aaa gta tgatttactt atcaactctt             1700
172 Thr Met Ile Lys Thr Tyr Leu Lys Val
173                   520
175 aggtttgtgt atatatatgt tgatttatct gaataatcga tcaaagaatg gtatgtgggt     1760
177 tactaggaag ttggaaacaa acatgtatag aatctaagga gtgatcgaaa tggagatgga     1820
179 aacgaaaaga aaaaaatcag tcttttgtttt gtggttagtg                          1860
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 524
184 <212> TYPE: PRT
185 <213> ORGANISM: Arabidopsis thaliana
187 <400> SEQUENCE: 2
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189 1               5                   10                  15
191 Phe Pro Ser Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr
192               20                  25                  30
194 Ser Tyr Arg Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly
195         35                  40                  45
197 Gly Gly Ser Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe
198       50                  55                  60
200 Ala Asp Glu Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe
201 65                  70                  75                  80
203 Val Gln Met Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val
204               85                  90                  95
206 Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val
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RAW SEQUENCE LISTING   DATE: 01/23/2001
PATENT APPLICATION: US/09/701,395   TIME: 11:13:18

Input Set : A:\108172-00022.txt
Output Set: N:\CRF3\01232001\I701395.raw

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207            100                105                110
209 Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala
210        115                120                125
212 Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr
213     130                135                140
215 Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln
216 145                150                155                160
218 Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp
219             165                170                175
221 Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg
222        180                185                190
224 Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser
225         195                200                205
227 Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu
228     210                215                220
230 Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala
231 225                230                235                240
233 Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val
234             245                250                255
236 Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu
237         260                265                270
239 Val Glu Asn Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr
240     275                280                285
242 Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro
243 290                295                300
245 Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu
246 305                310                315                320
249 Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys
250             325                330                335
252 Thr Lys Leu Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys
253         340                345                350
255 Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro
256     355                360                365
258 Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val
259 370                375                380
261 His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro
262 385                390                395                400
264 Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys
265             405                410                415
267 Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro
268         420                425                430
270 Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu
271     435                440                445
273 Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe
274     450                455                460
276 Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
277 465                470                475                480
279 Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
280             485                490                495
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RAW SEQUENCE LISTING   DATE: 01/23/2001
PATENT APPLICATION: US/09/701,395   TIME: 11:13:18

Input Set : A:\108172-00022.txt
Output Set: N:\CRF3\01232001\I701395.raw

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282 Pro Asn Asn Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro
283              500               505               510
285 Thr Gly Ala Thr Met Ile Lys Thr Tyr Leu Lys Val
286              515               520

288 <210> SEQ ID NO: 3
289 <211> LENGTH: 956
290 <212> TYPE: DNA
291 <213> ORGANISM: Arabidopsis thaliana
293 <400> SEQUENCE: 3
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296 tctctccgtc tcttcgattt aaacgctttt ctgtctgtta cgtcgtcgaa gaacggagac    120
298 agaattctcc gattgagaac gatgagagac cggagagcac gagctccaca aacgctatag    180
300 acgctgagta tctggcgttg cgtttggcgg agaaattgga gaggaagaaa tcggagaggt    240
302 ccacttatct aatcgctgct atgttgtcga gctttggtat cacttctatg gctgttatgg    300
304 ctgtttacta cagattctct tggcaaatgg agggagggtga gatctcaatg ttggaaatgt    360
306 ttggtacatt tgctctctct gttggtgctg ctgttggtat ggaattctgg gcaagatggg    420
308 ctcatagagc tctgtgtgca gcttctctat ggaatatgca tgagtcacat cacaaaccaa    480
311 gagaaggacc gtttgagcta aacgatgttt ttgctatagt gaacgctggt ccagcgattg    540
313 gtctcctctc ttatggattc ttcaatanag gactcgttcc tggtctctgc tttggcgccg    600
315 ggttaggcat aacggtgttt ggaatcgcct acatgtttgt ccacgatggt ctcgtgcaca    660
317 agcgtttccc tgtaggtccc atcgccgacg tcccttacct ccgaaaggtc gccgccgctc    720
319 accagctaca tcacacagac aagttcaatg gtgtaccata tggactgttt cttggaccca    780
321 aggaattgga agaagttgga ggaaatgaag agttagataa ggagattagt cggagaatca    840
323 aatcatacaa aaaggcctcg ggctccgggt cgagttcgag ttcttgactt taaacaagtt    900
325 ttaaatccca aattctttt ttgtcttctg tcattatgat catcttaaga cggtct    956
327 <210> SEQ ID NO: 4
328 <211> LENGTH: 294
329 <212> TYPE: PRT
330 <213> ORGANISM: Arabidopsis thaliana
332 <400> SEQUENCE: 4
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334  1               5               10               15
336 Leu Ser Gly Phe Ser Pro Ser Leu Arg Phe Lys Arg Phe Ser Val Cys
337              20               25               30
339 Tyr Val Val Glu Glu Arg Arg Gln Asn Ser Pro Ile Glu Asn Asp Glu
340              35               40               45
342 Arg Pro Glu Ser Thr Ser Ser Thr Asn Ala Ile Asp Ala Glu Tyr Leu
343      50               55               60
345 Ala Leu Arg Leu Ala Glu Lys Leu Glu Arg Lys Lys Ser Glu Arg Ser
346  65               70               75               80
348 Thr Tyr Leu Ile Ala Ala Met Leu Ser Ser Phe Gly Ile Thr Ser Met
349              85               90               95
351 Ala Val Met Ala Val Tyr Tyr Arg Phe Ser Trp Gln Met Glu Gly Gly
352              100               105               110
354 Glu Ile Ser Met Leu Glu Met Phe Gly Thr Phe Ala Leu Ser Val Gly
355              115               120               125
357 Ala Ala Val Gly Met Glu Phe Trp Ala Arg Trp Ala His Arg Ala Leu
358      130               135               140
360 Trp His Ala Ser Leu Trp Met Asn His Glu Ser His His Lys Pro Arg
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Use lower-case letters for bases, when using new Sequence Rules format. Please correct globally.

<210> 13
<211> 960
<212> DNA
<213> Tagetes erecta

<400> 13

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TGGATGCTGT TCAGCGACGT CTCATGTTTG ACGATGAATG CATTTTGGTG GATGAGTGTG   120

ACAATGTGGT GGGACATGAT ACCAAATACA ATTGTCACTT GATGGAGAAG ATTGAAACAG   180

GTAAAATGCT GCACAGAGCA TTCAGCGTTT TTCTATTCAA TTCAAAATAC GAGTTACTTC   240

TTCAGCAACG GTCTGCAACC AAGGTGACAT TTCCTTTAGT ATGGACCAAC ACCTGTTGCA   300

GCCATCCACT CTACAGAGAA TCCGAGCTTG TTCCCGAAAC GCCTGAGAGA ATGCTGCACA   360

GAGGANNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   420

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   480

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   540

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   600

NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN   660

NNNNNNNNNN NNNNNNNNNN TCATGTGCAA AAGGGTACAC TCACTGAATG CAATTTGATA   720

TGAAAACCAT ACACAAGCTG ATATAGAAAC ACACCCTCAA CCGAAAAGCA AGCCTAATAA   780

TTCGGGTTGG GTCGGGTCTA CCATCAATTG TTTTTTTCTT TTAACAACTT TTAATCTCTA   840

TTTGAGCATG TTGATTCTTG TCTTTTGTGT GTAAGATTTT GGGTTTCGTT TCAGTTGTAA   900

TAATGAACCA TTGATGGTTT GCAATTTCAA GTTCCTATCG ACATGTAGTG ATCTAAAAAA   960
```

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

also see item 10 on Err. Summary Sheet

Input Set : A:\108172-00022.txt
Output Set: N:\CRF3\01232001\I701395.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=1
L:294 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=3
L:554 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=9
L:594 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=10
L:636 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=11
L:684 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=12
L:729 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=13
L:741 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:741 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:741 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:741 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:741 M:340 W: (46) "n" or "Xaa" used: Feature required for SEQ ID#:13
L:743 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:743 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:745 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:745 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:745 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
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L:747 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
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L:751 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:1341 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=22
L:1521 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=24
L:1634 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:25
L:1634 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25

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L:1634 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1634 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:25
L:1634 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1743 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
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L:1743 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1743 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1840 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=28
L:1881 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=29
L:1931 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=30
L:1975 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=31
L:2015 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=32
L:2055 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=33
L:2125 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=34
L:2163 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=35
L:2782 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=46
L:3019 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:48
L:3019 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
L:3019 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
L:3019 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:48
L:3019 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:48
```